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GenCore version 5 1 3 Copyright (c) 1993 - 2003 Compugen 15d
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OM protein - protein search, using sw model

Jacuary 19, 2003, 16,40 32, Sepred Line 40 0714 Sergads Pun on.

(Without alignments) 56.562 Million cell updates/sec

US-09-856-070-23 1 ELMLRLQDYEE 11 Perfect score Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched.

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:* Database :

sp_hacteria:* sp_archea:*

sp_unclassitied:*
sp_rvirus:* sp_invertebrate:* sp_vertebrate:* sp_mammal:*
sp_mhc:*
sp_organelle:* sp_rodent:* sp_phage: * sp_plant: * sp_virus:* sp_fungi:* sp_human:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_bacteriap:*

sp_archeap:*

SUMMARIES

		*				
Result. N∩	Score	Query M atch	Query Match Length DR	PR	ID	Description
: :	55	100.0	586	+	096008	096cu8 homo sanion
C4	 64	94.5	50 60 60	-	<u>0</u> 90JZ6	Ogrité homo sabien
÷	52	 ₹	SAF	Ξ	291711	redrift nus muscula
4	50	6.06	158	4	090JZ7	Oguiz7 homo sapien
S	48	87.3	455	Π	CRVHK3	Osebka rattus nerv
9	40	7.2.7	R. 92.	~	9MUA60	Cordwe dallus dall
7	3.0	70.0	429	~	P78514	978514 homo sarice
ထ	39	70.9	453	4	099854	099854 homo sapien
σ	38	70.9	634	Φ	09XJS3	09xis3 bacteriopha
10	ъ́£	70.9	802	4	ppayou	Ogy699 homo sapien
11	38	69.1	130	16	Q9K660.	Jukeho bacillus ha
12	38	1.69	150	16	Q8UHE2	OBuhe2 agrobacteri
۲.	37	67.3	1111	S.	064106	O64106 bacteriopha
4	37	67.3	1111	16	034838	034838 bacillus su
15	3.7	67.3	C3	-+	080102	OSala2 pyrococus
16	37	67.3	231	1	080008	ORUĐVA BYDOS

159 AA.

PRT;

PRELIMINARY;

Q9uuz6 ID Qquuz6

RESULT 2

Q8t9v0 aedes aegyp	Ofpas2 xylella fas	C66941 aquifex aco	Q91480 salmo salar					09k728 bacillus ha	warral streptomyce		Q8svc8 encephalito	QBrcx7 thermoanaer	Q8t3h6 drosophila	Q9vp18 drosophila	O81465 arabidopsis	Quoxy5 fuga rabrip	098uif cyprinus ca	Q9btnl homo saplen	091sa4 arabidopsis	O29591 archaeoglob	O44141 oryza sativ			Q9d5q0 mus musculu		Q9eq58 mus musculu		Q91km6 zea mays (m
081900	0.9PG\$2	066941	091480	Q9H742	Q923U1	Q9PAP4	09:748	Q9K728	OSKIST	Q97FF3	Q8SVC8	Q8P○X7	Q8T3H6	Q9VP1.8	081465	Q90XY5	098016	Q9BTN1	Q9LSA4	029541	_044H41	049177	Q94F17	0,000	QSHRUÜ	Q9FQ58	Q9EQ57	9€.78
R)	16	16	13	<u>ب</u>	10	16	13	16	ئے	16				ιΩ	10	۳.	13	4	10	7	_	10	10	17	17	1]	Ξ	10
363	321	337	1058	250	784	338	45.4	99	7.5	221	942	080	418	443	477	7 : 4	754	25.8	1298	105	150	181	186	235	250	294	314	321
					65.5			63.6		63.6			9.89	63.6	63.6	63.6	63.6	63.6	63.6			61.8	61.8	61.8	61.8		61.8	
3.7	1.7	27	3.7	36	36	36	9	35	3.5	35	3.5	io M	35	35	35	35	35	d) m	35	3.4	34	3.4	34	34	34	34	34	34
17	σ: -1	J. 1	2.0	2.1	CI CI	23	: # : 1	25	2,	27	58	<u>ග</u> රෘ	30	3.1	3.5	3.3	34	\$3 \$5	36	53	38	3.5	4 0	4.1	42	43	44	4.5

ALIGNMENTS

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sdeb to
                                                                                                             Similar to villin 2 (ezrin).
Inno sapiens (Human).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Frimates; Catarrhini; Hominidae: Homo.
                                                                                                                                                                                                                                             Strausberg R.;
Submitted (SFF 2001) to the EMHI/GenHank/DDHJ databases.
Submitted (SFF 2001) to the EMHI/GenHank/DDHJ databases.
EMHI, HC013903 AAH13903.1;
InterPro: IPR000299; Hand_4.1.
R InterPro: IPR000798; EZ/ad/moesin.
Pram; PF00759; EMH. 1.
R PROSTIE: PS00660; HAND_411.1; UNKNOWN_1.
PPROSTIE: PS00660; HAND_411.2; UNKNOWN_1.
PPROSTIE: PS00661; HAND_411.3; 1.
SEWIENCE SUB AA: P9412 MW; t1B5920149AA/CG46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Shore 55; DB 4; Length 586; 160.0%; Pred. No. 0.034; Cive. 0; Mismatches 0; Indels
                                                           01-DEC-2001 (ГРЕМИЛГО! 19, Created)
01-DEC-2001 (ТРЕМИЛГО! 19, Last sequence update)
01-MAR-2002 (ТРЕМИЛГО! 20, Last ancotation update)
                                 PRI;
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Matches 11, Conservative 0;
                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ELMLRLQDYEE 11
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                 NCB1_Tax1D-9606;
                                                                                                                                                                                                                                     TISSUE-COLON;
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                                               Q96CU8;
                          996008
RESULT 1
               9950UB
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A RULINE 21085660; PubMed 11217851;

A RAWAI J., Shinagawa A., Shihataa K., Yoshino M., Itoh M., Ishii Y.,

A Andawa I., Shinagawa A., Shihataa K., Yoshino M., Itoh M., Ishii Y.,

A Alakawa I., Hara A., Pukunishi Y., Konno H., Adachi J., Pukuda S.,

A Alawa K., Ishwa M., Nishi N., Kiposawa H., Kondo S., Yamanaka I.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rudota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rudota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rudota R., Matsuda H., Nikaido I., Pesole G., Quackenbush J.,

Ashrimi I.M., Staubii F., Saruki P., Fomita M., Waquer I., Washio T.,

Sakai K., Okido T., Purnoo M., Aono H., Haddarelli R., Harsh G.,

Andrine J., Moltelli D., Rojumqu N., Carninci P., de Ronaldo M.F.,

Rrownstein M.J., Bult C., Pletcher C., Fujila M., Garibolii M.,

Androne P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Androne P., Ring B., Kingwald M., Rodriguez I., Sakamoto N.,

Androne P., Ring B., Kingwald M., Rodriguez I., Sakamoto N.,

Androne P., Ring B., Kingwald M., Rodriguez I., Sakamoto N.,

Androne P., Ring B., Kingwald M., Rodriguez I., Sakamoto N.,

Androne R., Sato K., Scheenbach C., Seya T., Shbata Y., Storch

Androne R., Sato K., Scheenbach C., Seya T., Shbata Y., Storch

Androne R., Sato K., Scheenbach C., Seya T., Shbata Y., Storch

Androne R., Sato K., Scheenbach C., Seya T., Shbata Y., Storch

Androne R., Sato K., Scheenbach C., Seya T., Shbata Y., Storch

Androne R., Sato K., Scheenbach C., Seya T., Shbata Y., Storch

Androne R., Sato K., Scheenbach C., Seya T., Shbata Y., Storch

Androne R., Sato K., Scheenbach C., Seya T., Shbata Y., Storch

Androne R., Sato K., Scheenbach C., Seya T., Kawaji H., Kohlsuki S.,

Androne R., Sato K., Scheenbach C., Seya T., Kawaji H., Kohlsuki S.,
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                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Enkaryota, Metassa, Chandata, Vertebaata, Esteleostomi,
Mammalia; Entheria; Primates, Catarrhini, Hominidae; Homo.
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Mammalia; Eutheria; Rodentia, Sciuroguathi, Muridac, Murinac, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse \mbox{collection.}^n; Nature 409:685-690(2001).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
4dult male kidney cDNA, RIKEN Full-length enriched library, clone-0610037422, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.5%; Score 52; DB 4; Length 159; 90.9%; Pred. No. 0.034; High I: Miccalches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.

Fadiel A., Chen Z.C., Nattolin F.,
"Mutation of ezrin gene in cancer.";
Submitted (SEP-1999) to the EMBL/GenBauk/DDBJ databases.
EMHL; AF189213; AAF03156.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 AA; 19244 MW; 70398388878A70FA CRC64;
                                        01 MAY-2000 (TrEMBLE). 13, Created)
01 MAY-2000 (TrEMBLE). 13, Last sequence update)
01 MAK-2002 (TrEMBLE). 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR000299; Band_4.1.
InterPro: IPR000798; P>/rad/mocsin.
Plan; PR00769; ERW: 1.
PROSITE: PS50057; BAND_41_3; 1.
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                                                                                                                                                                                                                       Ezrin (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_Tax1D-9606;
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NON_TER
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InterPro; IPR000299; Band_4.1.

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Eufeleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Rominidae: Romo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.9%; Score 50; DB 4; Length 158; 100.0%; Pred. No. 0.082;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY;
Gunn-Moore F.J., Tait S., Brophy P.J.;
Submitted (MOV-2001) to the EMBL/GenGank/DDBJ databases.
EMBL: AF450298; AAL47644.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen Z.C., Fadiel A., Naftolin F.; "Ezrin gene mutation in ovarian cancer."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                  PROSLIE: PS00e60; BAND_41_1; 1.
FROSLIE: PS00661; BAND_41_2; 1.
PROSLIE: PS00050; BAND_41_3; 1.
SEQUENCE: PS60057; 860434 MW; 591AA8F575F6DERE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation apdate)
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InterPro; PP0007249; Rand_4.1.
Fram, Fr0709; Ex/rad/mucsin.
Fram, Fr0709; ERM; 1.
PROSITE: PS50057; BAND_41_3; 1.
InterPro; 1Pk000798; Ez/rad/moesin.
Ptam; PF00373; Band_41; 1.
Pfam; PF00769; FRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                             PRINIS; PR00935; BAND41.
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                                                                                                                                                                    SMART; SM00295; B41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FLMLRLQDYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ezrin (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158
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EMBL. J. Neurosci. 11:549-71:
InterPro: IPR000299; Band_4.1.
InterPro: IPR000299; Band_4.1.
InterPro: IPR000373; Band_4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Verlebrata; Euteleostomi;
Archosauria; Aves; Necquathae; Galliformes; Phasianidae; Phasianinae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.3%, Score 48, DB 11, Length 455, 81.8%; Pred, No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; indels
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PROSITE: PS00661: BAND_41_2: 1.
PROSITE: PS50055: BAND_41_3: 1.
SEQUENCE: 585 AA: 69366 MW: R54C6348P7R3CARC CHC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 455 AA; 54174 MW; 1FC9A95F4C7D5893 CRC64,
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last ashotation update)
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D-MAY-1997 (TEMBLEAL. 03, Created)
01-MAY-1997 (TEMBLEC) 03 Last sequence update)
01-MAY-1997 (TEMBLEC) 03 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      585 AA.
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                                                                                                                                                                                                                                                                                   SMART; SM00295; B41; 1.
PROSITE: PS00669. BAND_41_1, UNKNOWN_1.
PPROSITE: PS00661: BAND_41_2; UNKNOWN_1.
PROSITE: PS00064: BAND_41_3; 1.
NON_FER 455 455
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Interpro- TPP000299, Rabi_4 1
Interpro: TPR000798; E2/rad/moesin.
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                                                                                                    Pfam; PF00373; Band_41; 1.
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SMART: SM00295; R41; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 ELMLRLQDFEQ 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FILMIRIQUYPE 11
                                                                                                                                                                         Pfam; PF00769; EKM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "fostinesal candidates for the FPB retinitis pigmentosa gene.";
Simitted (JAN 1997) to the FMRL/Conkank/ENET databases.
EMBL: U87408; AAB47568.1; c.
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"Purification and protein composition of PM2, the first lipid-
containing bacterial virus to be isolated.";
Virology 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.9%; Score 39; DB 4; Length 453; 72.7%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                      70.9%, Score 39, DB 4, Tength 429; 72.7%; Pred. No. 29;
Mannalia, Eutheria, Frimates, Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                    1; indels
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                                                                                                                                  Submitted (FLB 1997) to the EMBL/GenBank/DDEJ databases.
EMRL, IR8596; AAR61919 1; -
EMBL, U85994; AAR61918 1; -
EMBL, U85997; AAR46606.1; -;
Hypothetical protein.
NON_TER.
                                                                                                                                                                                                                                                                         SEQUENCE 429 AA; 48092 MW; D8D2471A95971E9A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01 MAY-1397 (TrEMBLICE, 03, Created)
U-MAY-1997 (TrEMBLICE, 03, Last sequence update)
01-DEC-2001 (TrEMBLICE, 19, Last annotation update)
Hypothetical 51.1 kDa protein (Frayment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                            Local Similarity 72.7%;
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                1 ELMLRLQDYEE 11
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Best Local Similarity
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                                                                   SHOUENCE FROM N.A.
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                        NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE~SPLEEN;
                                                                                         TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keen T.J.;
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                                                                                                                 Keen T.J
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Q99854;
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Fuji E., Hirama C., Nakamura Y., Ogasawara N., Kuhata S.
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                    150 AA
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                                                                                                                                                                       Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                        Transcriptional regulator, AsnC family. Arm0740 OR AGR_C_1339.
                                                                   EMBL, AP001520, HAH07591.1; -.
InterPro, IPR004360, GIY_bleo_diox.
Pfam, PF00903, Glyoxalase; 1.
                                                                                                                                                                                                                                                                                                                     PPT:
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EMBL; AE008008; AAK86548.1; -
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                                                                                                                                                                       87.58;
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                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                           78 LRVODYEE 85
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                                                                                                                                                                                                                  Gaps
                                                                                                            Mannisto R.H., Kivela H.M., Paulin L., Bamford D.H., Bamford J.K.H., Submitted (MAY 1999) to the EMBL/GenBank/EDBJ databases.
EMBL: AP155037; AAD43543.1; -.
                        Mannisto R.H., Kivela H.M., Paulin L., Bamford D.H., Bamford J.K., "The complete genome sequence of PM2, the first lipid containing bacterial virus To Be isolated.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo Saptens (Human).
Eukaryeta: Metazoa; Cherdata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99236731; PubMed-10221542;
Adams A.E., Rosenblatt M., Suva L.J.;
"Identification of a novel parathyroid humone responsive gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C-125 / TOM 4153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Fakaki Y., Maeno G., Sasaki R., Masui N.,
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                                                                                                                                                                                     Score 39; DB 9; Length 634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.9%; Score 39; DB 4; Length 802,
                                                                                                                                                                                                                1; Indels
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                                                                                                                                          13543.1; -.
72094 MW; PCSCDD004PFR2506 CRC64;
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802 AA; 89844 MW; 3D7B534492C4CA92 CRC64;
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01-001-2000 (TEPMRITEL, 15, 18st sequence apdate)
01-MAR-2002 (TEBMBIREL, 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                               43;
                                                                                                                                                                                                                  3; Mismatches
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                                                                                                                                                                                               Pred. No.
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            MEDIINE-99434236; PubMcd-10502514;
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                                                                                                                                                                                     70.98;
                                                                                                                                                                                                 63.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human osteoblastic cells.";
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EMBL: AF095771; AAD25981.1;
                                                                  Virology 262:355-364(1999).
                                                                                                                                                                                                 Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                      275 ELMVRIRGYEE 285
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                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                        634 AA.
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Wood D.W., Sctubal J.C., Kaul R., Monks D.E., Kitajima J.P., Oktafa V.K., Zhou Y., Chen L., Wood G.E., Almoida N.F. Jr., Woo D., Chen Y., Paulsen J.T., Elsen J.A., Karp F.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyaviu T., Levy K. Li M., Janker G., Gillet W., Grant C., Kutyaviu T., Levy K., Li M., Wollelland E., Palmieri A., Shaymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Shang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon Kamm B., Liao L., Kim S., Hendlick C., Zhao E.Y., Dolan M., Nester E.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               o; caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the plant pathogen and biotechnology agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.1%; Score 38; DB 16; Length 150; 80.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                    69.18; Score 38; DB 16; Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                          Hypothetical protein, Complete proteome.
SEQUENCE 130 AA, 15271 MW, B39FEREED72DF09F GRG64;
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01-JUN-2002 (TREMBERGE, 21, Last sequence update)
01-JUN-2002 (TREMBERGE, 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agrobacterium tumefaciens (strain C58 / ATCC 33970)
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Job time : 41.0714 secs
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RA Arevedo V., Bertero M.G., Dessieres P., Bolotin A., Borchert S.,
RA Horriss K., Bourstor L., Brans A., Brann M., Brigholl S.C., Brook RA Brouillet S., Bruschi C. V., Caddwoll H., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi G. V., Caddwoll H., Capuano V., Daniel R.A.,
RA Choi S.K., Codani J.J., Commerten I.F., Cummings N.J., Daniel R.A.,
RA Denizot E., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Chian K.D., Errington J., Pabret C., Galiczi A., Galleron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galiczi A., Galleron N.,
RA Chisephi G., Guy B.J., Haga K., Haiceh J., Brrwood C.R., Herlart A.,
Ra Hilbert H., Holsaphel S., Hosono S., Hallo M.Fr., Itaya M., Jones L.,
RA Kobayashi Y., Komingstein G., Ercah S., Fumano M.,
RA Kobayashi Y., Komingstein G., Ercah S., Fumano M.,
RA Medina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Noback M.,
RA Moore D., O'Reilly M., Gydwa R., Gyiwara A., Gudaqa H., Park S.H.,
RA Researan E. Pujir P., Purmelle B., Porche M., Scholer F., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sckiguchi J., Sekowska A., Seror S.J., Serror P., Shin H.S., Soldo H.,
                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                              "The complete nuclectide sequence of the Bacillus subtilis SPbetac2
                                                                                                                                                              Viruses) dsbNA viruses, no RNA stage, Caudovirales, Siphoviridae.
NCBL_TaxID=66797;
                                                                                                                                                                                                                       Lazarevic V., Duesterhoeft A., Soldo B., Hilbert H., Mauel C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria: Firmicutes: Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
NCBI_TaxID-1423;
                                                                                                                                                                                                                                                                                                                                                67.3%; Score 37; DB 9; Length 111;
                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                   Submitted (Arg-1947) to the EMBL/GenEsak/DDET databases
EMBL: AF020713: AAC13066.1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                       111 AA; 12549 MW; F1886BECB44AF778 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last ancotation update)
                                                                                          (TremMirel 07, Last sequence update)
(TremMirel 19, Last annotation update)
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                                                     111 AA
                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Pred. No. 18;
                                                                             01-AUG-1998 (TrEMHLITEL, 07, Created)
                                                   PPT:
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                                                                                                                     Hypothetical 12 5 kPa protein.
                                                                                                                                                                                                                                                                                                                                                                63.68;
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                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 63.6
Matches 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                  PPELIMINARY:
                                                                                                                                                  Bacteriophage SPBc2.
                                                                                                                                                                                                                                                                                                                                                                                                        1 ELMLRLQDYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                   20 FLKLEISDYEE 30
                                                                                                                                                                                                      SEQUENCE FROM N.A.
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064106
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                       RESULT 13
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034838
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Sorokin A., Tarwoni E., Takada T., Tabahashi H., Takemaru K., Takeduchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tacato V., Chiyama S., Yaddehadi M., Vannier F., Vassaronti A., Viari A., Rambutt R., Wedler E., Wedler H., Weitzenegger T., Winter S., Wipat A., Yamamoto E., Yadua K., Yashida K., Yoshikawa H.E., Zumstein H., Yashikawa H., Danchin A., The complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea, Euryarchaeota, Thermococci, Thermococcales, Thermococcaceae;
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Weiss P R , Dunn D M . Pobb F.I., Brown J.R.;
"The complete sequence of the Pyronoccus furiosus genome.";
Submitted (FEB 2502) to the EMBL/GenBark/DDBJ databases.
EMBL; AE010221; AAJ81237.1; -
Hypothetical protein; Complete proteome.
SFGUENCE 217 AA; 24508 MW; 91F2538E57C38451 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Gength 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.3%; Score 37; DB 17; Length 217; 63.6%; Pred. No. 35;
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                                                                                                                                                                                                                                                                                                 Kunst F., ogasawata N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: 299114; CAB13966.1; -.
EMBL: 299115; CAB13992.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AA; 12549 MW; F1886HECB44AF778 CRC64;
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01.JUN-2002 (TREMBLrel. 21, Last. sequence update)
01.JUN-2002 (TREMBLrel. 21, Last annotation update)
Hypothetical protein PF1113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.3%; Score 37;
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Bost Local Similarity 63.00
Tr. Conservative
                                                                                                                                                                                                         Mature 390:249-256(1997).
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